

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=2; day=19; hr=10; min=35; sec=1; ms=967;]

=====

Reviewer Comments:

<220>

<221> VARIANT

<222> (297) ... (297)

<223> tyrosine, valine, isoleucine, leucine, methionine, phenylalanine, tryptophan

<400> 6

Arg Xaa Xaa Thr Xaa Ser Xaa Leu Thr Glu Xaa Xaa Xaa Xaa Gly Arg

1 5 10 15

Xaa Gln Xaa Xaa Glu Xaa Xaa Xaa Xaa Leu Leu Leu Xaa Xaa Xaa

20 25 30

Gly Xaa Xaa Xaa Phe Xaa Val Xaa Pro Xaa Val Gly Xaa Gly Gly Xaa

35 40 45

A mandatory feature is required to cover every "Xaa" used in a sequence. SEQ ID # 6 does not have a feature to cover the "Xaa" at positions 223. Please make all necessary changes.

Application No: 10573372 Version No: 2.0

Input Set:

Output Set:

Started: 2009-01-30 19:08:24.415
Finished: 2009-01-30 19:08:35.769
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 354 ms
Total Warnings: 5
Total Errors: 4
No. of SeqIDs Defined: 7
Actual SeqID Count: 7

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
E 341	'Xaa' position not defined SEQID (6) POS (223)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)

SEQUENCE LISTING

<110> Dale, James Langham
Echeverria, Santy Peraza

<120> BANANA RESISTANCE GENES AND USES THEREOF

<130> DAVI172.006APC

<140> 10573372
<141> 2009-01-30

<150> PCT/AU2004/001300
<151> 2004-09-23

<150> AU 2003905222
<151> 2003-09-25

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 4380
<212> DNA
<213> Musa acuminata

<220>

<221> CDS
<222> (1)..(4323)

<400> 1
atg tcg acg gcg cta gta atc gga gga tgg ttc gcg caa agc ttc atc 48
Met Ser Thr Ala Leu Val Ile Gly Gly Trp Phe Ala Gln Ser Phe Ile
1 5 10 15

cag acg ttg ctc gac aag gcc agc aac tgc gcg atc caa caa ctc gcg 96
Gln Thr Leu Leu Asp Lys Ala Ser Asn Cys Ala Ile Gln Gln Leu Ala
20 25 30

cgg cgc cgc ggc ctt cac gat gac ctg agg cgg ctg cgg acg tct ctg 144
Arg Arg Arg Gly Leu His Asp Asp Leu Arg Arg Leu Arg Thr Ser Leu
35 40 45

ctc cgg atc cat gcc atc ctc gac aag gca gag acg agg tgg aac cat 192
Leu Arg Ile His Ala Ile Leu Asp Lys Ala Glu Thr Arg Trp Asn His
50 55 60

aaa aac acg agc ttg gtg gag ctg gtg agg cag ctc aag gat gct gcc 240
Lys Asn Thr Ser Leu Val Glu Leu Val Arg Gln Leu Lys Asp Ala Ala
65 70 75 80

tat gac gcc gag gac tta ctg gag gag ttg gag tac caa gcc gcg aag 288

Tyr Asp Ala Glu Asp Leu Leu Glu Leu Glu Tyr Gln Ala Ala Lys			
85	90	95	
caa aag gtc gag cac cgg gga gac cag ata agc gac ctc ttt tct ttt			336
Gln Lys Val Glu His Arg Gly Asp Gln Ile Ser Asp Leu Phe Ser Phe			
100	105	110	
tcc ctt agt act gcg agc gag tgg ttg ggt gcc gat ggt gat gat gct			384
Ser Leu Ser Thr Ala Ser Glu Trp Leu Gly Ala Asp Gly Asp Asp Ala			
115	120	125	
ggg act cga ttg agg gag atc cag ggg aag ctg tgc aac att gct gcc			432
Gly Thr Arg Leu Arg Glu Ile Gln Gly Lys Leu Cys Asn Ile Ala Ala			
130	135	140	
gat atg atg gat gtc atg cag cta ttg gca ccc gat gat ggg ggg aga			480
Asp Met Met Asp Val Met Gln Leu Leu Ala Pro Asp Asp Gly Gly Arg			
145	150	155	160
caa ttc gac tgg aag gtg gtg aga aga gaa acg acg tct ttc ttg acc			528
Gln Phe Asp Trp Lys Val Val Arg Arg Glu Thr Ser Ser Phe Leu Thr			
165	170	175	
gaa acc gtc gtg ttt ggt cgg gac caa gaa agg gag aaa gta gta gaa			576
Glu Thr Val Val Phe Gly Arg Asp Gln Glu Arg Glu Lys Val Val Glu			
180	185	190	
ttg ctg ttg gat tca gga tct ggt aac agt agc ttc tct gtc tta ccc			624
Leu Leu Leu Asp Ser Gly Ser Gly Asn Ser Ser Phe Ser Val Leu Pro			
195	200	205	
ctc gtc gga atc gga ggg gtt ggg aag acg act ctg gct cag ctc gtg			672
Leu Val Gly Ile Gly Gly Val Gly Lys Thr Thr Leu Ala Gln Leu Val			
210	215	220	
tac aac gac aat cgt gtc ggc aac tat ttc cac ctc aag gtt tgg gtc			720
Tyr Asn Asp Asn Arg Val Gly Asn Tyr Phe His Leu Lys Val Trp Val			
225	230	235	240
tgt gta tcc gac aat ttc aat gtg aag aga ctg acc aaa gag ata atc			768
Cys Val Ser Asp Asn Phe Asn Val Lys Arg Leu Thr Lys Glu Ile Ile			
245	250	255	
gag tct gct acc aag gtg gaa caa tct gac aaa ttg aac ttg gac acc			816
Glu Ser Ala Thr Lys Val Glu Gln Ser Asp Lys Leu Asn Leu Asp Thr			
260	265	270	
ctg caa cag atc ctc aag gag aag att gct tca gag agg ttt ctg cta			864
Leu Gln Gln Ile Leu Lys Glu Lys Ile Ala Ser Glu Arg Phe Leu Leu			
275	280	285	
gtc ctc gat gat gtg tgg agc gaa aac agg gat gac tgg gaa agg ctg			912
Val Leu Asp Asp Val Trp Ser Glu Asn Arg Asp Asp Trp Glu Arg Leu			
290	295	300	
tgc gca cca cta agg ttt gca gca aga ggc agc aag gtt ata gtc aca			960
Cys Ala Pro Leu Arg Phe Ala Ala Arg Gly Ser Lys Val Ile Val Thr			

305	310	315	320	
act cga gac aca aag att gcc agc atc att ggc aca atg aag gaa att				1008
Thr Arg Asp Thr Lys Ile Ala Ser Ile Ile Gly Thr Met Lys Glu Ile				
325	330	335		
tcg ctc gat ggt ctc cag gat gct tac tgg gag ctg ttc aag aaa				1056
Ser Leu Asp Gly Leu Gln Asp Asp Ala Tyr Trp Glu Leu Phe Lys Lys				
340	345	350		
tgt gca ttt ggt tct gtg aac ccc cag gag cat cta gag ctc gag gtt				1104
Cys Ala Phe Gly Ser Val Asn Pro Gln Glu His Leu Glu Leu Glu Val				
355	360	365		
atc ggt aga aag att gct ggt aag ttg aag ggc tca ccg cta gca gca				1152
Ile Gly Arg Lys Ile Ala Gly Lys Leu Lys Gly Ser Pro Leu Ala Ala				
370	375	380		
aaa aca cta gga agc ttg ttg cgg ttg gat gtc agc caa gaa cac tgg				1200
Lys Thr Leu Gly Ser Leu Leu Arg Leu Asp Val Ser Gln Glu His Trp				
385	390	395	400	
aga act ata atg gaa agt gag gta tgg caa ctg cca caa gct gaa aat				1248
Arg Thr Ile Met Glu Ser Glu Val Trp Gln Leu Pro Gln Ala Glu Asn				
405	410	415		
gaa ata ttg cct gtt cta tgg ctg agc tat caa cac ctt ccc gga cat				1296
Glu Ile Leu Pro Val Leu Trp Leu Ser Tyr Gln His Leu Pro Gly His				
420	425	430		
ctt aga cag tgt ttc gct ttt tgc gct gtg ttt cac aaa gat tat tta				1344
Leu Arg Gln Cys Phe Ala Phe Cys Ala Val Phe His Lys Asp Tyr Leu				
435	440	445		
ttc tat aaa cat gag ttg atc cag act tgg att gca gaa ggc ttc att				1392
Phe Tyr Lys His Glu Leu Ile Gln Thr Trp Ile Ala Glu Gly Phe Ile				
450	455	460		
gca cat caa gga aac aag agg atg gaa gat gtc gga agc agc tac ttc				1440
Ala His Gln Gly Asn Lys Arg Met Glu Asp Val Gly Ser Ser Tyr Phe				
465	470	475	480	
cat gag ctt gtt aat agg tct ttc ttt cag gaa tct cgg tgg aga ggg				1488
His Glu Leu Val Asn Arg Ser Phe Phe Gln Glu Ser Arg Trp Arg Gly				
485	490	495		
cga tat gtg atg cat gac ctc ata cac gat ctt gcc caa ttt ata tca				1536
Arg Tyr Val Met His Asp Leu Ile His Asp Leu Ala Gln Phe Ile Ser				
500	505	510		
gtg gga gag tgt cat agg ata gat gat gac aag tcc aaa gag acc cct				1584
Val Gly Glu Cys His Arg Ile Asp Asp Asp Lys Ser Lys Glu Thr Pro				
515	520	525		
agt acg act cgt cat cta tca gta gca tta act gag caa atg aag ttg				1632
Ser Thr Thr Arg His Leu Ser Val Ala Leu Thr Glu Gln Met Lys Leu				
530	535	540		

gtg gat ttt tca ggt tac aat aaa ttg cgg acc ctt atg atc aac aat Val Asp Phe Ser Gly Tyr Asn Lys Leu Arg Thr Leu Met Ile Asn Asn 545	550	555	560	1680
cag aga aat cag tat cca tat atg act aaa gtc aac agc tgc ttg ttg Gln Arg Asn Gln Tyr Pro Tyr Met Thr Lys Val Asn Ser Cys Leu Leu 565	570	575		1728
cct cat agc ttg ttc aaa aga ctg aaa aga atc cat gtt tta gtt ttg Pro His Ser Leu Phe Lys Arg Leu Lys Arg Ile His Val Leu Val Leu 580	585	590		1776
cag aag tgt ggc atg aaa gag ttg cct gat att atc ggt gac ttg ata Gln Lys Cys Gly Met Lys Glu Leu Pro Asp Ile Ile Gly Asp Leu Ile 595	600	605		1824
caa ctt cgg tac ctt gac ata tcc tac aat gct tgc att cag agg ttg Gln Leu Arg Tyr Leu Asp Ile Ser Tyr Asn Ala Cys Ile Gln Arg Leu 610	615	620		1872
ccc gag tca ttg tgc gac ctt tac aat ctg caa gca ctg agg cta tgg Pro Glu Ser Leu Cys Asp Leu Tyr Asn Leu Gln Ala Leu Arg Leu Trp 625	630	635	640	1920
ggc tgt caa tta cgg agt ttc cca caa ggc atg agc aag ctg atc aac Gly Cys Gln Leu Arg Ser Phe Pro Gln Gly Met Ser Lys Leu Ile Asn 645	650	655		1968
ttg agg caa ctt cgt gta gaa gat gag ata att tcc aag ata tat gag Leu Arg Gln Leu Arg Val Glu Asp Glu Ile Ile Ser Lys Ile Tyr Glu 660	665	670		2016
gtt ggg aag ctg att tct ctg caa gaa ttg tct gca ttc aaa gtg cta Val Gly Lys Leu Ile Ser Leu Gln Glu Leu Ser Ala Phe Lys Val Leu 675	680	685		2064
aat aat cat gga aac aaa ctt gca gaa cta agt ggt ttg aca caa ctc Asn Asn His Gly Asn Lys Leu Ala Glu Leu Ser Gly Leu Thr Gln Leu 690	695	700		2112
cgc agc act cta cga att aca aat ctt gaa aat gta ggg agt aaa gaa Arg Ser Thr Leu Arg Ile Thr Asn Leu Glu Asn Val Gly Ser Lys Glu 705	710	715	720	2160
gaa gca agc aag gct aaa ctg cac agg aaa cag tat ctt gaa gca tta Glu Ala Ser Lys Ala Lys Leu His Arg Lys Gln Tyr Leu Glu Ala Leu 725	730	735		2208
gag tta gag tgg gca gct ggc cag gtt tcc agc ttg gag cat gag tta Glu Leu Glu Trp Ala Ala Gly Gln Val Ser Ser Leu Glu His Glu Leu 740	745	750		2256
ctt gtc tcg gag gaa gta ctt tta ggt ctc caa cca cat cac ttc ctc Leu Val Ser Glu Glu Val Leu Leu Gly Leu Gln Pro His His Phe Leu 755	760	765		2304

aaa agt ttg aca atc aga ggg tac agt ggt gca aca gta ccc agt tgg			2352
Lys Ser Leu Thr Ile Arg Gly Tyr Ser Gly Ala Thr Val Pro Ser Trp			
770	775	780	
ctg gat gtg aaa atg cta ccg aac ttg gga act ctt aaa cta gag aac			2400
Leu Asp Val Lys Met Leu Pro Asn Leu Gly Thr Leu Lys Leu Glu Asn			
785	790	795	800
tgt aca aga ctg gag ggt ctt tca tat att gga caa ctg cca cat ctc			2448
Cys Thr Arg Leu Glu Gly Leu Ser Tyr Ile Gly Gln Leu Pro His Leu			
805	810	815	
aag gtc ctt cat atg aag aga atg cct gtg gtg aaa caa atg agt cat			2496
Lys Val Leu His Met Lys Arg Met Pro Val Val Lys Gln Met Ser His			
820	825	830	
gaa tta tgt ggc tgt acg aaa agc aag ttg ttc cct agg cta gaa gag			2544
Glu Leu Cys Gly Cys Thr Lys Ser Lys Leu Phe Pro Arg Leu Glu Glu			
835	840	845	
tta gta ctg gag gat atg cca aca ttg aaa gaa ttc ccg aat ctt gca			2592
Leu Val Leu Glu Asp Met Pro Thr Leu Lys Glu Phe Pro Asn Leu Ala			
850	855	860	
caa ctt cct tgt ctc aag att att cac atg aag aac atg ttt gca gta			2640
Gln Leu Pro Cys Leu Lys Ile Ile His Met Lys Asn Met Phe Ala Val			
865	870	875	880
aaa cat ata ggt cgt gaa tta tat ggt gat ata gag agc aat tgt ttt			2688
Lys His Ile Gly Arg Glu Leu Tyr Gly Asp Ile Glu Ser Asn Cys Phe			
885	890	895	
cta tca tta gaa gag ctt gtg ctg cag gac atg ctg aca ttg gag gaa			2736
Leu Ser Leu Glu Leu Val Leu Gln Asp Met Leu Thr Leu Glu Glu			
900	905	910	
ctc cca aat ctt gga caa ctt cca cat ctt aag gtt att cac atg aag			2784
Leu Pro Asn Leu Gly Gln Leu Pro His Leu Lys Val Ile His Met Lys			
915	920	925	
aac atg tct gca ctg aaa ctt ata ggt cgt gaa tta tgt gat tct aga			2832
Asn Met Ser Ala Leu Lys Leu Ile Gly Arg Glu Leu Cys Asp Ser Arg			
930	935	940	
gag aaa att tgg ttt cct agg cta gaa gtg cta gtg ctg aag aac atg			2880
Glu Lys Ile Trp Phe Pro Arg Leu Glu Val Leu Val Leu Lys Asn Met			
945	950	955	960
ctg gca ctg gag gaa ctc cca agc ttg gac aac ttc cgt gtc tca aga			2928
Leu Ala Leu Glu Leu Pro Ser Leu Asp Asn Phe Arg Val Ser Arg			
965	970	975	
ttc ttc gca tcc agt gtc gaa gta ggc cat gga ctc ttt agt gct acg			2976
Phe Phe Ala Ser Ser Val Glu Val Gly His Gly Leu Phe Ser Ala Thr			
980	985	990	
agg aat aaa tgg ttt cca agg ctg gaa gag cta gaa atc aag ggc atg			3024

Arg Asn Lys Trp Phe Pro Arg Leu Glu Glu Leu Glu Ile Lys Gly Met			
995	1000	1005	
ctg aca ttt gag gaa ctc cat tct ctt gaa aaa ctg cca tgt ctc			3069
Leu Thr Phe Glu Glu Leu His Ser Leu Glu Lys Leu Pro Cys Leu			
1010	1015	1020	
aag gtt ttc cgc atc aag gga ttg cca gca gtg aaa aag ata ggc			3114
Lys Val Phe Arg Ile Lys Gly Leu Pro Ala Val Lys Lys Ile Gly			
1025	1030	1035	
cat gga tta ttt gat tct acc tgt cag aga gag tgt ttt cca agg			3159
His Gly Leu Phe Asp Ser Thr Cys Gln Arg Glu Cys Phe Pro Arg			
1040	1045	1050	
ttg gaa gat ctc gta tta agc gac atg cca gca tgg gaa gag tgg			3204
Leu Glu Asp Leu Val Leu Ser Asp Met Pro Ala Trp Glu Glu Trp			
1055	1060	1065	
tcg tgg gct gaa agg gag gag tta ttt tcc tgc ttg tgt aga ctt			3249
Ser Trp Ala Glu Arg Glu Glu Leu Phe Ser Cys Leu Cys Arg Leu			
1070	1075	1080	
aaa att gaa caa tgc ccc aaa ctt aaa tgc ttg ctt ccc atc cct			3294
Lys Ile Glu Gln Cys Pro Lys Leu Lys Cys Leu Leu Pro Ile Pro			
1085	1090	1095	
cat tct ctc ata aaa ctt gaa tta tgg caa gtt ggg ctg aca gga			3339
His Ser Leu Ile Lys Leu Glu Leu Trp Gln Val Gly Leu Thr Gly			
1100	1105	1110	
ctt cca gga tta tgc aaa gga att ggt gga ggt agc agc act aga			3384
Leu Pro Gly Leu Cys Lys Gly Ile Gly Gly Ser Ser Thr Arg			
1115	1120	1125	
act gct tct ctc tca ctc ttg cac att att aaa tgt cca aat ctg			3429
Thr Ala Ser Leu Ser Leu Leu His Ile Ile Lys Cys Pro Asn Leu			
1130	1135	1140	
aga aat ctg gga gaa ggg ttg cta tca aac cac ctg cca cat atc			3474
Arg Asn Leu Gly Glu Gly Leu Leu Ser Asn His Leu Pro His Ile			
1145	1150	1155	
aat gct att cgg ata tgg gaa tgt gct gaa ctg ttg tgg ctg cct			3519
Asn Ala Ile Arg Ile Trp Glu Cys Ala Glu Leu Leu Trp Leu Pro			
1160	1165	1170	
gtc aag agg ttt aga gaa ttc acc acc ctt gag aac ttg tca ata			3564
Val Lys Arg Phe Arg Glu Phe Thr Thr Leu Glu Asn Leu Ser Ile			
1175	1180	1185	
agg aac tgc ccc aag ctc atg agc atg aca cag tgt gag gag aat			3609
Arg Asn Cys Pro Lys Leu Met Ser Met Thr Gln Cys Glu Glu Asn			
1190	1195	1200	
gac ctc ctc ctc ccg ccg tta atc aag gca cta gaa ttg ggt gac			3654
Asp Leu Leu Leu Pro Pro Leu Ile Lys Ala Leu Glu Leu Gly Asp			

1205

1210

1215

tgt gga aat ctt ggg aaa tcg ctg cct gga tgc cta